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Tumor-intrinsic pathway activation associated with the non-T cell-inflamed tumor microenvironment

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Tumors With Substantial Susceptibility to Anti-PD1 Antibody (partial list...)

FDA approved:

- Melanoma
- Non-Small Cell Lung Cancer
- Renal Cell Carcinoma Clear Cell
- Urothelial Cancer
- Hodgkin's Lymphoma
- Head and Neck Squamous Carcinoma
- Merkel Cell Carcinoma
- Mis-Match Repair Deficient Colorectal Carcinoma
- Gastroesophageal Cancer
- Hepatocellular Carcinoma

Registrational trial on-going

- Mesothelioma
- Triple-Negative Breast Cancer
- Small Cell Lung Cancer
- Ovarian Cancer
- Glioblastoma



Luke et al. Oncotarget 2015

Working Model: Immunobiology of T cell-inflamed & Non-Inflamed Tumor Microenvironment



Ribas et al. J Clin Oncol 33, 2015 (suppl; abstr 3001)

What Are the Molecular Mechanisms That Explain the T Cell-Inflamed vs. Non-Inflamed Tumor Microenvironments?



- 1. Somatic differences at the level of tumor cells
 - Mutational landscape and antigenic repertoire
 - Distinct oncogene pathways activated in different patients
- 2. Germline genetic differences at the level of the host
 - Polymorphisms in immune regulatory genes
- 3. Environmental differences
 - Commensal microbiota
 - Immunologic/pathogen exposure history

Workflow Identifying WNT/β-catenin Signaling Between T Cell-Inflamed & Non-T Cell-Inflamed Melanoma



β-catenin Represses CCL4, Leading to Lack of Batf3⁺ DC Recruitment, Failed T cell Priming, and Non-Response to Checkpoint Blockade





Genetic Landscape of the T Cell-Inflamed Tumor Microenvironment Across TCGA Solid Tumors

UCS

UVM



LIHC

LUAD

PRAD

READ

COAD

GBM

Cancer Type	Non-inflamed	Int	Inflamed	Total
30 solid	3000	2873	3017	8890
primary tumors	(32.7%)	(32.3%)	(33.9%)	

Spranger and Luke et al. PNAS 2016



Gene expression score

Spranger and Luke et al. PNAS 2016

The Lack of T Cell Infiltration is Unique to Non-Inflamed Tumor Microenvironment Relative to Matched Normal



Non-T cell-inflamed tumors show lower gene immune gene expression score relative to normal tissue controls (p=1.10e-111) T cell-inflamed tumors showed a significantly higher gene expression score relative to normal tissue (p=2.23e-106).



Mechanisms of β -catenin pathway activation interrogated in non-T cell-inflamed tumors

- Mutation
 - Activating mutations CTNNB1
 - Inactivating mutations in negative regulators
 - Axin1, Axin2, APC1, APC2
- Pathway activation without mutations
 - E.g. overexpression of Wnt ligands, Fzd receptors, βcatenin itself





Location of literature annotated β-catenin mutations

CTNNB1 all non-synonymous mutations (451 mutations total; 253 muttions within exon 3)



Frequency of β-catenin pathway mutations in non-T cell-inflamed tumors



Note that this is likely an underestimate as few mutations are well characterized outside of exon 3



Difference of β-catenin mutated patients between non-T cellinflamed and inflamed tumor groups per cancer



16 tumors show β-catenin activation as greater in non-T cellinflamed versus T cell-inflamed tumor groups



activated patients in tumor group



Difference in percentage of activated patients between tumor groups

Inverse correlation between β-catenin protein level and T cell-inflamed gene expression



Select list of therapeutics to target β-catenin

Small molecules

- E7386 (Eisai CREB-binding protein/β-catenin transcription activation complex)
- PRI-724 (Prism Biolabs CREB-binding protein)
- BC-2059 (Beta-cat Pharma Transducin β-like 1)
- Preclinical Venn Therapuetics
- Macrocyclic scaffolds
 - Preclinical (Circle Pharma)
- Stapled peptides
 - Preclinical (Fogpharma)
 - Preclinical (WntRx)
- Antibody drug conjugates
 - Preclinical to clinic (Several)





Yamada *et al.* AACR 2017 – abstract 5177 El-Khoueiry *et al.* ASCO 2013 – 2501 Savvidou et al. Mol Cancer Ther. 2017

Beyond β-catenin: PTEN Loss in Melanoma Associates with Non-T Cell-Inflamed Tumor Microenvironment and Resistance to anti-PD-1



Beyond Melanoma: FGFR3 Expression Present in Non-T Cell-Inflamed Bladder Cancer



Phase I study of FGFR inhibitor in combination with anti-PD1 in FGFR3 expressing tumors in development!



	<u>Non-T cell-inflamed</u> <u>(n= 76)</u>		<u>T cell-inflamed</u> (n =85)				
Gene	Samples	Variants	Samples	Variants			
FGFR3	11	14	0	0			
	Non-T cell-inflamed		T cell	T cell-inflamed			
Gene Fusion	Sa	Samples		Samples			
FGFR3-TACC3		3	0				
4000- E 3000- E 2000-			 → Jax-MB49-FGFR3^{G370C} PBS → Jax-MB49-2G PBS → Jax-MB49-FGFR3^{G370C} anti-PD-L1 → Jax-MB49-2G anti-PD-L1 				
ັດ ມີ 1000-			P = 0.016 (2-way ANOVA)				
0 10	15 20 Days	²⁵ Sweis	et al. Cancer Immunol Res. 2016 Sweis unpublished				

Genes enriched for somatic mutations in non-inflamed compared to inflamed tumors



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Top Ranked Genes Are Known to Drive Immune Exclusion or Involved in Immune System Regulation



Top Ranked Genes Are Known to Drive Immune Exclusion or Involved in Immune System Regulation



Top Genes Associated With Non-T Cell-Inflamed Microenvironment by Tumor Type



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Amino Acid Changes Associated With Non-T Cell-Inflamed Microenvironment





Amino Acid Level Changes Associated With Non-T Cell-Inflamed Microenvironment



Treatment with IDH-C35 improves the efficacy of peptide vaccines in mice bearing GL261-MUT tumors





Phase I/II study of IDH1 inhibitor AG-120 and nivolumab in IDH1 mutant advanced solid tumors

Agios IST-2017-10170 in collaboration with BMS





Activated signaling pathways correlated with non-T cellinflamed tumor microenvironment





Immune subtypes correlate with genome state





Thorrson et al. Immunity 2018

Impact of oncogenic signaling on immune inhibitory pathways and cell populations





Wellenstein and de Visser KE. Immunity. 2018

Conclusions

- T cell-inflamed tumor microenvironment may serve as a model for predicting molecular pathways associated with immune inclusion vs exclusion phenotype
- Several tumor-intrinsic signaling pathways associated and have been mechanistically shown to drive the non-T cellinflamed phenotype
 - Somatic alterations in other pathways may additionally be of relevance: IDH, βcatenin, PTEN, RAS, FGFR3 etc.
- Clinically validated biomarkers of transcriptional activation
 needed but may present rational IO combintaion targets



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